



SEQUENCE LISTING

<110> Kato, Seishi
Sekine, Shingo

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND
CDNAS ENCODING THESE PROTEINS

<130> 1997.17300.2

<140> 10/616,942

<141> 2003-07-11

<150> 09/529,100

<151> 2000-08-21

<150> JP 0276269

<151> 1997-10-08

<150> PCT/JP98/04474

<151> 1998-10-05

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<170> PatentIn Ver. 2.0

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Leu Tyr Ile Gly Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu
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Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys
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Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg
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 Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
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 Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
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 Ala Ser Val Ala Gly Leu Thr Ala Ala Tyr Arg Val Thr Leu Asn
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ccaagggagc aggacggagc c atg gac ccc gcc agg aaa gca ggt gcc cag 111
                        Met Asp Pro Ala Arg Lys Ala Gly Ala Gln
                        1          5          10
gcc atg atc tgg act gca ggc tgg ctg ctg ctg ctg ctt cgc gga 159
Ala Met Ile Trp Thr Ala Gly Trp Leu Leu Leu Leu Leu Arg Gly
                        15          20          25
gga gcg cag gcc ctg gag tgc tac agc tgc gtg cag aaa gca gat gac 207
Gly Ala Gln Ala Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp
                        30          35          40
gga tgc tcc ccg aac aag atg aag aca gtg aag tgc gcg ccg ggc gtg 255
Gly Cys Ser Pro Asn Lys Met Lys Thr Val Lys Cys Ala Pro Gly Val
                        45          50          55
gac gtc tgc acc gag gcc gtg ggc gcg gtg gag acc atc cac gga caa 303
Asp Val Cys Thr Glu Ala Val Gly Ala Val Glu Thr Ile His Gly Gln
                        60          65          70
ttc tcg ctg gca gtg cgg ggt tgc ggt tcg gga ctc ccc ggc aag aat 351
Phe Ser Leu Ala Val Arg Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn
                        75          80          85
gac cgc ggc ctg gat ctt cac ggc ctt ctg gcg ttc atc cag ctg cag 399
Asp Arg Gly Leu Asp Leu His Gly Leu Leu Ala Phe Ile Gln Leu Gln
                        95          100          105
caa tgc gct cag gat cgc tgc aac gcc aag ctc aac ctc acc tcg cgg 447
Gln Cys Ala Gln Asp Arg Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg
                        110          115          120
gcg ctc gac ccg gca ggt aat gag agt gca tac ccg ccc aac ggc gtg 495
Ala Leu Asp Pro Ala Gly Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val
                        125          130          135
gag tgc tac agc tgt gtg ggc ctg agc cgg gag gcg tgc cag ggt aca 543
Glu Cys Tyr Ser Cys Val Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr
                        140          145          150
tcg ccg ccg gtc gtg agc tgc tac aac gcc agc gat cat gtc tac aag 591
Ser Pro Pro Val Val Ser Cys Tyr Asn Ala Ser Asp His Val Tyr Lys
                        155          160          165
ggc tgc ttc gac ggc aac gtc acc ttg acg gca gct aat gtg act gtg 639
Gly Cys Phe Asp Gly Asn Val Thr Leu Thr Ala Ala Asn Val Thr Val
                        175          180          185
tcc ttg cct gtc cgg ggc tgt gtc cag gat gaa ttc tgc act cgg gat 687
Ser Leu Pro Val Arg Gly Cys Val Gln Asp Glu Phe Cys Thr Arg Asp
                        190          195          200
gga gta aca ggc cca ggc ttc acg ctc agt ggc tcc tgt tgc cag ggc 735
Gly Val Thr Gly Pro Gly Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly
                        205          210          215
tcc cgc tgt aac tct gac ctc cgc aac aag acc tac ttc tcc cct cga 783
Ser Arg Cys Asn Ser Asp Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg
                        220          225          230
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atc cca ccc ctt gtc cgg ctg ccc cct cca gag ccc acg act gtg gcc 831
 Ile Pro Pro Leu Val Arg Leu Pro Pro Pro Glu Pro Thr Thr Val Ala
 235 240 245 250
 tca acc aca tct gtc acc act tct acc tcg gcc cca gtg aga ccc aca 879
 Ser Thr Thr Ser Val Thr Thr Ser Thr Ser Ala Pro Val Arg Pro Thr
 255 260 265
 tcc acc acc aaa ccc atg cca gcg cca acc agt cag act ccg aga cag 927
 Ser Thr Thr Lys Pro Met Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln
 270 275 280
 gga gta gaa cac gag gcc tcc cgg gat gag gag ccc agg ttg act gga 975
 Gly Val Glu His Glu Ala Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly
 285 290 295
 ggc gcc gct ggc cac cag gac cgc agc aat tca ggg cag tat cct gca 1023
 Gly Ala Ala Gly His Gln Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala
 300 305 310
 aaa ggg ggg ccc cag cag ccc cat aat aaa ggc tgt gtg gct ccc aca 1071
 Lys Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr
 315 320 325 330
 gct gga ttg gca gcc ctt ctg ttg gcc gtg gct gct ggt gtc cta ctg 1119
 Ala Gly Leu Ala Ala Leu Leu Leu Ala Val Ala Ala Gly Val Leu Leu
 335 340 345
 tgagctttctc cacctggaaa tttccctctc acctacttct ctggccctgg gtacccctct 1179
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 ttccccagta tccccagctt ctgctgcgct ggtttgccgc tttgggaaat aaaataccgt 1299
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<210> 22
 <211> 346
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala
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 Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu
 20 25 30
 Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
 35 40 45
 Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
 50 55 60
 val Gly Ala val Glu Thr Ile His Gly Gln Phe Ser Leu Ala val Arg
 65 70 75 80
 Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
 85 90 95
 His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
 100 105 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
 115 120 125
 Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
 130 135 140
 Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
 145 150 155 160
 Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
 165 170 175
 Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
 180 185 190
 Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
 195 200 205
 Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
 210 215 220
 Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
 225 230 235 240
 Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr
 245 250 255
 Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
 260 265 270
 Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
 275 280 285
 Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
 290 295 300
 Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
 305 310 315 320
 Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
 325 330 335
 Leu Leu Ala Val Ala Ala Gly Val Leu Leu
 340 345

<210> 23
 <211> 781
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (342)..(539)

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 aaagcggcgg cgacggcggc gcgagaacga cccggcggcc agttctcttc ctctgcgca 120
 cctgccctgc tcggtcagtc agtcggcggc cggcgccccg cttgtgctca gacctcgcgc 180
 ttgcggcgcc caggcccagc ggccgtagct agcgtctggc ctgagaacct cggcgctccg 240

ggggaattcg agga

14

<210> 26
<211> 162
<212> PRT
<213> Homo sapiens

<400> 26
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30
Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
35 40 45
Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
50 55 60
Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
65 70 75 80
Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
85 90 95
Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
100 105 110
Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
115 120 125
Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
130 135 140
Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
145 150 155 160
Lys Gln

<210> 27
<211> 162
<212> PRT
<213> Homo sapiens

<400> 27
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30
Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
35 40 45
Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
50 55 60
Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
65 70 75 80

Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
 85 90 95
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
 100 105 110
 Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
 115 120 125
 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
 130 135 140
 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
 145 150 155 160
 Lys Gln

<210> 28
 <211> 64
 <212> PRT
 <213> Nematode

<400> 28
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 1 5 10 15
 Asn Val Asn Asn Arg Gly Asn Val Ala Lys Ser Leu Lys Pro Ala Glu
 20 25 30
 Asp Lys Tyr Pro Ala Ala Pro Trp Leu Ile Gly Leu Phe Val Phe Val
 35 40 45
 Val Cys Gly Ser Ala Val Phe Glu Ile Ile Arg Tyr Val Lys Met Gly
 50 55 60

<210> 29
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 29
 Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
 1 5 10 15
 Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
 20 25 30
 Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
 35 40 45
 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
 50 55 60
 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
 65 70 75 80
 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
 85 90 95
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
 100 105 110

Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
 115 120 125
 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
 130 135 140
 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
 145 150 155 160
 Lys Gln

<210> 30
 <211> 185
 <212> PRT
 <213> Nematode

<220>
 <221>
 <222> 150
 <223> Unknown

<400> 30
 Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
 1 5 10 15
 Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
 20 25 30
 Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
 35 40 45
 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
 50 55 60
 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
 65 70 75 80
 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
 85 90 95
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
 100 105 110
 Cys Glu His Phe Val Asn Glu Leu Met Ala Pro Lys Gln Arg Met Thr
 115 120 125
 Leu Ala Asn Lys Gln Phe Ser Lys Asn Val Asn Asn Arg Gly Asn Val
 130 135 140
 Ala Lys Ser Leu Lys Xaa Pro Ala Glu Asp Lys Tyr Pro Ala Ala Pro
 145 150 155 160
 Trp Leu Ile Gly Leu Phe Val Phe Val Val Cys Gly Ser Ala Val Phe
 165 170 175
 Glu Ile Ile Arg Tyr Val Lys Met Gly
 180 185